Additional file 5: Fig. S2.

Nanopore methylation analysis allow to distinguish disease samples from controls and other diseases samples (t-SNE).

t-SNE scatter plot from methylation levels at Sotos, Kabuki, Wiedemann-Steiner (WDSTS) and Cornelia de Lange (CdLS) syndromes episignature loci. Nanopore sequencing data of five healthy controls and seven patients with one of the four disorders are represented, along with the array-based reference [5] for the respective episignature. Patients sequenced with nanopore cluster in close proximity to their respective array-based episignature reference.